What is claimed is:

1. A method of screening test subjects to identify those more likely to have better growth, development, reproduction and carcass traits such as rates of gain, carcass length, or litter size, comprising: obtaining a sample of genetic material from a test subject and assaying for the presence of a polymorphism in the CYP11a1 gene which is associated with rate of gain, carcass length, and litter size.

2. The method of claim 1 wherein said step of assaying is selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP), denaturing gradient gel electrophoresis (DGGE) and temperature gradient gel electrophoresis (TGGE).

3. The method of claim 1, wherein said step of assaying for the presence of said polymorphism comprises the steps of digesting said genetic material with a restriction enzyme that cleaves the CYP11a1 gene in at least one place; separating the fragments obtained from the said digestion; detecting a restriction pattern generated by said fragments; and comparing said pattern with a second restriction pattern for the CYP11a1 gene obtained by using said restriction enzyme, wherein said second restriction pattern is associated with increased rates of gain, increased carcass length, and increased litter size.

4. A method as claimed in claim 1, wherein said test subject is selected from the group consisting of pigs, cows and chickens.

5. The method of claim 3 wherein said restriction enzyme is SphI and said test subject is a pig.

6. The method of claim 3 wherein said separation is by gel electrophoresis.

7. The method of claim 3 wherein said step of comparing said restriction patterns comprises identifying specific fragments by size and comparing the sizes of said fragments.

8. The method of claim 5 further comprising the step of amplifying the amount of porcine CYP11a1 gene or a portion thereof which contains said polymorphism, prior to said digestion step.

9. The method of claim 3 wherein said restriction site is located in the untranslated region of the CYP11a1 gene.

10. The method of claim 7 wherein said amplification includes the steps of selecting a forward and a reverse sequence primer capable of amplifying a region of the porcine CYP11a1 gene which contains a polymorphic restriction site.

11. The method of claim 10 wherein said forward and reverse primers are between 10 and 50 nucleotides in length and selected from SEQ ID NO: 1.

12. The method of claim 10 wherein said forward primer is SEQ ID NO:2 and said reverse primer is SEQ ID NO:3.

13. The method of claim 6 wherein said step of

detecting sizes of said fragments comprises the steps of separating said fragments by size using gel electrophoresis in the presence of a control DNA fragment of known size; contacting said separated fragments with a probe that hybridizes with said fragments to form probe-fragment complexes; and determining the size of separated fragments by detecting the presence of the probe fragment.

14. A method for identifying a genetic marker for pig growth rate, carcass length, litter size, or boar taint comprising the steps of breeding male and female pigs of the same breed or breed cross or derived from similar genetic lineages; determining the growth rates, carcass lengths, number of offspring, or presence of boar taint; determining the presence of a polymorphism in the CYP11a1 gene of each pig; and associating the growth rate, carcass length, number of offspring, or presence of boar taint of each pig with said polymorphism thereby identifying a polymorphism for these traits.

15. The method of claim 14 further comprising the step of selecting pigs for breeding which are predicted to have better growth rates, longer carcasses, increased litter size, or decreased boar taint by said marker.

16. The method of claim 14 wherein said analysis comprises digestion of PCR amplified DNA with the restriction enzyme SphI.

17. The method of claim 12 wherein said polymorphism associated with growth rate, carcass length, litter size, or boar taint is detected by use of forward and reverse primers comprising at least 4

consecutive bases in SEQ NOS: 2 and 3.

18. A kit for evaluating a sample of porcine DNA comprising, in a container, a reagent that identifies a polymorphism in the porcine CYP11a1 gene.

19. The kit of claim 18 wherein said reagent is a primer that amplifies the porcine CYP11a1 gene or a fragment thereof.

20. The kit of claim 18 further comprising a DNA polymerase, a restriction enzyme which cleaves the porcine CYP11a1 gene in a least one place; and forward and reverse primers capable of amplifying a region of the porcine CYP11a1 gene which contains a polymorphic site.

21. A primer for assaying for the presence of a polymorphic SphI site in the porcine CYP11a1 gene wherein said primer comprises a sequence from the group of SEQ ID NO:2 and SEQ ID NO:3.

22. A genetic marker associated with growth rate, carcass length, litter size, and boar taint in pigs, said marker comprising a polymorphism in the porcine CYP11a1 gene.

23. The genetic marker of claim 22 wherein said polymorphism is a SphI restriction site.

24. The marker of claim 22 wherein said polymorphism is located in the 5' untranslated region of the porcine CYP11a1 gene.

25. A DNA sequence from the porcine CYP11a1 gene 5'

untranslated region, said sequence consisting of SEQ ID NO: 1.

26. A primer designed to amplify a polymorphic SphI restriction site in the porcine CYP11a1 gene wherein said primer is 4 or more continuous bases from SEQ ID NO: 1.

27. A primer designed to amplify a polymorphic SphI restriction site in the porcine CYP11a1 gene wherein said primer is a reverse primer generated from the SEQ ID NO: 1.

28. A method for screening pigs to determine those more likely have increased growth rates, longer carcasses, larger litters, higher boar taint, and/or those less likely to exhibit increased growth rates, longer carcasses, larger litters, or higher boar taint, which method comprises of the steps: determining the alleles of the CYP11a1 gene present in a pig; determining the alleles of other markers for genes know to affect growth rate, carcass length, litter size, or boar taint; and selecting for animals with favorable combinations of alleles and against those carrying unfavorable combinations.

29. The method of claim 28 wherein the determination of CYP11a1 alleles comprises determining the presence of at least one allele associated with at least one DNA marker linked either directly or indirectly to CYP11a1.

30. The method of claim 28 wherein the DNA marker is a microsatellite.

31. The method of claim 28 wherein the DNA marker is SO064, SO102, S0078, SO158, S0066, SW304, SW1083, SO101, or S0212.

32. The method of claim 28 wherein the marker is selected from the group of tumor necrosis factor alpha (TNFα), CYP11a1, prolactin (PRL), estrogen receptor (ER) and prolactin receptor (PRLR).